OM protein - protein search, using sw model

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August 21, 2001, 12:06:43; Search time_11.18 Seconds

(without alignments)
962.095 Million cell updates/sec

Run on:

Sequence: Title: perfect score:

US-09-486-334-2

MATCIDTCRTGNTQDDDSRF......IPCLTMDQTSYLTEWSDYV1 314

Scoring table:

BLOSUM62

Searched:

Total number of hits satisfying chosen parameters:

93435 seqs, 34255486 residues Gapop 10.0 , Gapext 0.5

93435

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_39:*

score

d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

Result o.

Match

Length DB

CYSE_ECOLI

P05796 escherichia P29847 salmonella

buchnera ap

synechococc

haemophilus

synechocyst staphylococ bacillus su

azotobacter

Description

CYSE_HAEIN CYSE_SALTY Query

648.5 Score

420.5 399 369.5 365 359 287

CYSE_HELPJ SRPH_SYNP7

WCAB_ECOLI NODL_RHILV YA64_METJA

CYSE_HELPY NIFP_AZOCH

P23145 P71405 Q9zk14 Q59967 P77558

P08632 Q58464 P07464

methanococc escherichia synechococc

escherichia rhizobium l helicobacte helicobacte

saccharomyc rhizobium m schizosacch

CYSE_SYNY3 CYSE_BACSU CYSE_SYNP7 CYSE_BUCAP CYSE_BUCA1

430

NODL_RHIME

P40892 Q09707 P28266 Q9zed3 P37515

150 146.5 136.5 133.5 129.5 127.5

MAA_ECOLI LPXD_RICRI TABB_PSESZ

2 aquifex aeo 2 pseudomonas

escherichia bacillus su rickettsia

rickettsia

THGA_LACLA LPXA_AQUAE

WCAF_ECOL Y304_METJA

LPXA_YEREN LPXA_HAEIN LPXA_PROMI

yersinia

haemophilus proteus mir

escherichia methanococc staphylococ lactococcus

120 117.5 115.5 115 115

160 156.5 153.5 217 164.5 164.5

39.5 38.1 38.1 38.5 38.5 38.5 26.2 25.6 25.6 26.2 24.3 22.5 22.5 22.6 23.6 23.6 23.6 24.6 25.6 26.6

Minimum DB seq length: Maximum DB seq length:

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seq length:

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RESULT 1
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01-NOV-1988 (Rel. 09, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "L-cysteine biosynthesis in Escherichia coli: nncleotide sequence and expression of the serine acetyltransferase (cysE) gene from the wild-type and a cysteine-excreting mutant."; type and a cysteine-excreting mutant. ". Gen. Microbiol. 133:515-525(1987).
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STRAIN-KL2 / MG1655;
STRAIN-KL2 / MG1655;
MEDLINE-9431650; PubMed-8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
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                                                                                          MEDLINE=20085066; PubMed=10617639; Shaw W.V.; Moody P.C., Rowe A.J., Shaw W.V.; *Serine acetyltransferase from Escherichia coli is a dimer of trimers."; J. Biol. Chem. 275:461-466(2000).
                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDLINE=91099514; PubMed=2125278;
  -!- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
-!- PATHWAY: CYSTEINE BIOSYNTHESIS.
-!- SUBUNIT: HOMOHEXAMER. DIMER OF A HOMOTRIMER.
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CAT4_ECOLI
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p17114 escherichia
p50870 enterococcu
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Submitted (MAY-1991) to the EMBL/GenBank/DDBJ
SEQUENCE FROM N.A. Rogers G.E.;
                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                            STRAIN-LT2
                                                                                                                                                   Salmonella_typhimurium
                                                                                SEQUENCE FROM N.A.
                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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P29847;
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine blosynthesis; Repeat.
SEQUENCE 273 AA; 29316 MW; 466EB898750EF709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNQ 123
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PIR; A34563; A34563.
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SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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                                                                                                                                                                                                                                            273 AA.
                                       Rogers G.E.;
                       databases.
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                           SEQUENCE FROM N.A.
STRAIN-RD / RW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-NOV-1996 (Rel. 39, Last annotation update)
SBRINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
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                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                        Haemophilus influenzae.
                                                                                                   NCBI_TaxID=727;
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

Transferase; Acyltransferase; Cysteine blosyuthesis; Repeat.

SEQUENCE 273 AA; 29291 MW; 6A5736E656FBD25B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNK 123
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-!- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
-!- PATHMAY: CYSTEINE BIOSYNTHESIS.
-!- SUBUNIT: HOMOHEXAMER. DIMER OF A HOMOTRIHER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACCETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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Patent number GB2227243, 25-JUL-1990.
-!- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
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51.2%; Pred. No. 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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Pfam; PF00132; hexapep; 2.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

PROSITE; PS00101; HEXAPEP_TRANSFERASE; Cysteine biosynthesis; Repeat.

Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.

SECURENCE 267 AA; 29166 MW; 93428DE9D504DFB4 CRC64;

SECURENCE 267 AA; 29166 MW; 93428DE9D504DFB4 CRC64;
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                                                                                                                                                                 CYSE_BUCAI
P57162;
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SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                             01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last seq
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                                                                                           SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT)
                                                                                                                                                                                                                                                                                                                                                                                                                               124
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                 Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                     symbiotic bacterium)
                                                   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                  241
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(Rel. 40, Last annotation update)
                                                                                                                                                                                         STANDARD;
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48.48; Pred. No. 2.4e-42;
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                                                                                                                                                                                                 PRT;
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Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
Nature 407:81-86(2000).
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SEQUENCE FROM N.A.
STRAIN-TOKYO 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 27steine biosynthesis; Repeat.

Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.

Transferase; Acyltransferase; 535055 MW; 5530252F10488681 CRC64;

PROFESSOR OF TRANSFERASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP001118; BAB12777.1;
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                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Schizaphis gramiուտ»).
Bacteria; Proteobacteria; gamma subdivision; Huchnera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 -SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI 283
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                                                       CYSE, and SecB.";
Gene 119:113-118(1992).
-i- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=93012960; PubMed=1398077;
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SIMILARITY: BELONGS TO THE CYSE/LACA/LPX1/NODL FAMILY OF
                                                                                                                                          endosymbiont of aphids) containing genes homologous
                                                                                                                                                                         Lai C.-Y., Baumann P.;
"Sequence analysis of a DNA fragment from Buchnera aphidicola (an
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
      -!- PATHWAY: CYSTEINE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 IWNKILYDVSFILKKEPILSDFYOSSILOHOSFTSSLSYILSNKLSTSMISEKKIOGIFD 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSQNRHPTIRKGVVIGAGAKILGNIEVGSGAKIGAGSIVLKNVPSDVTVVGVPAKIV 245
                                        SERINE
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                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-96281517; PubMed-8661945;

Anandan S., Nalty M.S., Cogdell D.E., Golden S.S.;

"Identification of two classes of transcriptional regulator genes in the cyanobacterium Synechococcus sp. strain PCC 7942.";

Arch. Microbiol. 166:8-63(1996).

-i- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
                      -!- PATHWAY: CISTAIN BECOME

-!- SUBCELULAR LOCATION: CYTOPLASMIC (BY SINILARITY).

-!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF

ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                              -!- PATHWAY: CYSTEINE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                          056002;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                 Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JC1493, UC1491; IRRO01451; -.
InterPro; IPRO01451; -.
Pfam; PF00132; hexapep; 2.
PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
Transferase; Acyltransferase; DC02685464A25944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 KENPRKH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 QSG-DRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGG 285
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-!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.18;
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44.1%; Pred. No. 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
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RESULT 7
CYSE_BACSU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                    Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                      "Clustering and co-transcription of the Bacillus subtilis genes encoding the aminoacyl-trNA synthetases specific for glutamate for cysteine and the first enzyme for cysteine biosynthesis.", Biol. Chem. 269:7473-7482(1994)
                                                                                                                                                                                                                                                                   MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gagnon Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=94171772; Pubmed=7510287;
                                                                                                                                                                                                                                                                                                                                                                                                              Lapointe J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q06750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AGAKVLGNIQIGENVRIGAGSVVLRDVPSDCTVVGIPGRV (YRSGVRVDPLDHSOMP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; SEQUENCE 244 AA; 26453 MW; AB0B50491023EDB1 CRC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 AGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL1----GGKENPRKHDKIP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                  SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                          SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                                  PATHWAY: CYSTEINE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 IHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 DLIAVKERDPACISYVHCELGEKGPLACQAHRIAHTLWKQVRKIVALLIQNRVSESFAVD 182
                                                                                                                                                                             CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L41665; AAB38543.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 DERIIFERDEAARNGLEVLLCYPGFQALVCHRVAHWLYQQRLPVIPRLLSHLSRLLTGVE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THÞGÁRLGÓGÍFIÐHGMGVVÍGETAIVGDYCLÍYQGVTLG FRKÓSGKRHPTLANNVVVG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Breton R., Putzer H., Pelchat M., Grunberg-Manago M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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48.0%;
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Pred. No. 4.4e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 AA.
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                                                                                                                                                                     COA + O-ACETYL-L-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajina N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z99104; CAB11869.1; -.
PIR; B53402; B53402.
HSSP; P01246; 1BST.
SubtiList; BG10155; cysE.
InterPro; IPR001451; -.
Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP; TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; ReSEQUENCE 217 AA; 24143 MW; 14EFA32FA1086D9D CRC64;
                                                                                                                                                                                                                                 "Sakamoto T., Wada H., Nishida I., Ohta H., Murata N.;
"Sequence analysis of a DNA fragment from Synechocystis PCC6803
containing genes homologous to cysE (serine acetyltransferase) and pgi
(glucose-6-phosphate isomerase).";
Plant Mol. Biol. 29:187-187(1995).
                                                                                                                                                                                                                                                                                                                                                                                                             P74089; Q55209;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803). Bacteria; Cyanobacteria; Chroococcal
                                                                                                                                                                                                                                                                                                                                                                                     SERINE ACETYLTRANSFERASE CYSE OR SLR1348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYSE_SYNY3
                                                                                                                                                                                        MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1148;
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   SUBCELLULAR
                                            CATALYTIC ACTIVITY:
                                                             Res.
                PATHWAY: CYSTEINE
                              SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIEIHPGATIGRRFFIDHGMGVVIGETCEIGNNVTVFQGVTLGGTGKEKGKRHPTIKDDA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDPVADRFKSLEQ 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D26185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                          3:109-136(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.8%;
               BIOSYNTHESIS
                                            ACETYL-COA +
                                                                                                                                                                                                                                                                                                                                                       Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                  (EC 2.3.1.30)
 CYTOPLASMIC (BY
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Pred. No. 1
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                                            L-SERINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                                  (SAT)
                                                                                                                                                                                                                                                                                                                                                       Synechocystis
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..2e-26;
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   SIMILARITY)
                                                                        protein-coding regions.";
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                                            COA +
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                                            O-ACETYL-L
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                                                                                    the
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RESULT 9
CYSE_STAXY
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         CYSE_STAXY P77985;
                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat.)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00132; hexapep; 3.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1
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                                                                                                                                                 FEMS
                                                                                                                                                               xylosus.
                                                                                                                                                                                             Fiegler
                                                                                                                                                                                                          STRAIN=DSM 20267 / C2A;
MEDLINE=97237691; PubMed=9084146;
                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                  Staphylococcus xylosus
Bacteria; Firmicutes; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
CONFLICT 80 80 I -> S (IN REF. 1).
SEQUENCE 249 AA; 27336 MW; ED5EC58D659DCFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D13777; BAA02919.1; -. EMBL; D90912; BAA18167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                            "Identification of the serine acetyltransferase
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=1288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001451; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
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                                                                                      PATHWAY: CYSTEINE BIOSYNTHESIS.
SUBCELLULAR LOCATION: CYTOPLASMIC
                                                      SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-x(4).
                                                                                                                                CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                             Brueckner R.;
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Bioinformatics
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                                                                                                                                  148:181-187(1997).
Y: ACETYL-COA + L-SERINE
                                                                                                                                                                                                                                                                                                   Bacillus/Clostridium
                                                                                                                                                                                                                                                                                   group;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                Staphylococcus
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RESULT
NIFP_A
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Best Local
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01-NOV-1991
01-JUN-1994
                           modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      Evans D.J., Jones R., Woodley P.R., Wilborn J.R., Robson R.L.;

"Nucleotide sequence and genetic analysis of the Azotobacter chroococcum nifusywzm gene cluster, including a new gene (nifp) encodes a serine acetyltransferase.";

J. Bacteriol. 173:5457-5469(1991).

-- FUNCTION: PROBABLE SERINE ACETYLTRANSFERASE REQUIRED FOR OPTIMIZING THE EXPRESSION OF NITROGENASE ACTIVITY. NIFP MAY REQUIRED TO BOOST RATES OF SYNTHESIS OR INTRACELLULAR CONCENTRATIONS OF CYSTEINE OR METHIONINE.
EMBL;
                                                                                                                       This
                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=91358323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZOCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00132; hexapep; 2.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.

Transferase; Acyltransferase; Cysteine biosynthesis; R
SEQUENCE 216 AA; 24000 MW; 728FE804A0D7282C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y07614; CAA68887.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      Azotobacter
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Azotobacter chroococcum
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                                                                                       European Bioinformatics Institute.
                                                                                                                                               SERINE.
SIMILARITY: BELONGS
ACETYLTRANSFERASES.
                                                                                                                                                                                           CATALYTIC ACTIVITY:
                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIGDNVLIAAGAKVLGNITINANVNIGANSVVLNSVPSYSTVVGIPGHIV--KQDGRRIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTFDHRNLPDPIYEQLKELEKQLEKTRNGEIQDDYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HDKIPCLTMDQTSYLTE------WSDYVI 314
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м60090;
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 AAA22162.1;
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                                                                                                                                                                                                                                                                                                                                            PubMed=1885524;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision; Pseudomonadaceae;
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(EC 2.3.1.30)
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                                                                                                                                               REPEATS OF [LIV]-G-X(4).
                                                        Usage
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                                                                                                                                                                                             COA + O-ACETYL-L-
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RESULT 11
CYSE_HELPY
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STRAIN-26695 / AFCC 700392;

MEDLINE-97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.

Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Sill S., Dougherty

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Sill S., Dougherty

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wal

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSE_HELPY
P71405;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 49503 / 60190;
Peek R.M., Thompson S.A., Atherton J.C., Blass
Peek R.M., Thompson S.A., atherton J.C., Blass
Pexpression of a novel ulcer-associated gene,
Texpression of a nov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Nitrogen fixation; Transferase; Acyltransf
Cysteine biosynthesis.
SEQUENCE 269 AA; 28578 MW; E0BBCC982E6
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                                                                                                                                                                                    pylori.
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01-OCT-2000
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                                                                                                                                                                   Nature 388:539-547(1997)
                                                                                                                                                                                                                                          Venter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                           PATHWAY: CYSTEINE BIOS
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                     SERINE
                                                                                                                                        CATALYTIC
                        ACETYLTRANSFERASES.
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                                                                                                                                                                                                             complete genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pylori (Campylobacter pylori)
                                                                                                                                           ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                        BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY FERASES. COMPOSED OF MULTIPLE REPEATS OF [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. 35, Created)
.. 35, Last sequence upda
.. 40, Last annotation up
ansferase (EC 2.3.1.30)
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                                                                                                                                                                                                               sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190
                                                                                          BIOSYNTHESIS
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                                                                                                                                 ACETYL-COA + L-SERINE =
                                                                      CYTOPLASMIC (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 369.5;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EOBBCC982E66FDBB
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                                                                                                                                                                                                             gastric
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                     REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                 pathogen Helicobacter
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                                                                                                                                           COA +
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                                                                                                                                           O-ACETYL-L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ.
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Wallin E
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Acyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Urla-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYSE OR JHP1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYSE_HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99120557; PubMed=9923682;
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                              gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence comparison of two unrelated isolates of the human
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                                                                                                                                                                       SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
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pr00132; hexapep; 2.
TE; pS00101; HEXAPEP_TRANSFERASES; 1.
TE; pS00101; HEXAPEP_TRANSFERASES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U43917; AAB07027.1; -.
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                                                                                                                                                                                                                                                                            PATHWAY: CYSTEINE BIOSYNTHESIS
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162 S
; 18342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.2%;
       institutions as long
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K -> R (IN STRAIN 60190).
S -> T (IN STRAIN 60190).
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Pred. No. 4.1e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28646D539C2250C3 CRC64;
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              as its content
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                              RESULT 13
SRPH_SYNP7
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Pfam; PF0013; hexapep; 4.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
Transferase; Acyltransferase; 2872B7539C3AC14A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001541; AAD06715.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SERINE ACETYLTRANSFERASE, PLASMID (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        059967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRPH_SYNP7
                                                                                                                                                                                                                                                                                                                                                                                  a cyanobacterial plasmid.";
Mol. Gen. Genet. 247:623-632(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 VKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPG 186
                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                             "Two enzymes together capable of cysteine biosynthesis are encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholson M.L., Gaasenbeek M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pANL.
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                       -!- PATHWAY: CYSTEINE BIOSYNTHESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95327059; PubMed=7603442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 VLGAICVGDDVRIGANAVVLSDLPTGSTAVGAKAKTI 167
               Transferase; Acyltransferase;
                            PROSITE; PS00101; HEXAPEP_TRANSFERASES;
                                                   InterPro; IPR001451; -.
Pfam; PF00132; hexapep; 2.
                                                                                      EMBL; U23436; AAA86726.1; -.
                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 ILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 VLQEDPAARNKWEVLLLYPGIHALLCYRLAHALHKRRFYFIARALSQLARFITGIEIHPG·70
SEQUENCE
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                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIGAGSC 246
                                                                                                                                                                                                                                                                                                                                                                                Gen.
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 319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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   34570 MW;
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Pred. No. 1.2e-21;
 Cysteine biosymhesis;
00BB74D8AABB1m70 CRC6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319
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                                          FALSI: NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                           D.E.;
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                        Repeat;
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Query Match

17.5%;

Score 287;

DB 1:,

Length 319

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RESULT 14
WCAB_ECOLI
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                                                                     Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., "A 460-kb DNA seguence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.", DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            STRAIN-KI / MG1655;

STRAIN-KI / MG1655;

STRAIN-KI / MG1655;

BIDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                      MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.; "Organization of the Escherichia coli K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid."; J. Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96326333; PubMed=8759852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOY-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
PUTATIVE COLANIC ACID BIOSYNTHESIS ACETYLTRANSFERASE WCAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 SESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGG-----TGK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 LLDS---DVNAAYLGDPAAQSISEILFCYPGITAITFHRLAHRLYQLGLPLLARITAEVS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 IIESTKODLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRV 175
                                   PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCHARIDE COLANIC ACID.
                    SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 HYFIGNTLDKTLNLLNEQIRRELWLQHVTQGTPEATPAVLSQHASELTQAFAQALPEIKR 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSIVSALSQASTDPLPHHLLSDQFY-PLPSRESLGLILHGLRSVLFPRHFGDPELSVETT 77
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      acetyl transferases
             Downie J.A.;
"The nodL gene from Rhizobium leguminosarum j
                                                         SIMILARITY TO OTHER MEMBER OF THE CYSE/LACA/NODL FAMILY
                                                                                            leguminosarum biovar viciae.";
Plant Mol. Biol. 13:163-174(1989).
                                                                                                                                    Canter Cremers H.C.J., Spaink H.P., Wijfjes A.H.M., Pees E., Wijffelman C.A., Okker R.J.H., Lugtenberg B.J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
NODULATION PROTEIN L (EC 2.3.1.-).
                                                  MEDLINE=90136094; PubMed=2615659
                                                                                                                                                                       MEDLINE=92003664; PubMed=2562395;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                  involved in efficient host-specific nodulation. Mol. Microbiol. 2:173-183(1988).
                                                                                                                                                                                                                                       Surin B.P., Downie J.A., "Characterization of the Rhizobium leguminosarum genes nodLMN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _RHILV
                                                                                                                        "Additional nodulation genes on the
                                                                                                                                                                                                                                                                                MEDLINE=88246045; PubMed=3132583;
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                        Plasmid sym
                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium leguminosarum (biovar viciae).
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NODL_RHILV P08632;
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00132; hexapep; 2.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; SEQUENCE 162 AA; 17615 MW; F2462F836F3FB3AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D90843; BAA15911.
EcoGene; EG13570; wcaB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 IGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AHRIAH--TLWKQ-----NRKIVALLIQNRVSES--FAVDIHPGAKIGKGILLDHATGVV 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 INKNVVAGDDFTIRHGVTIGNRGADN-MACPHIGNGVELGANVIILGDITLGNNVTVGAG
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      encoded
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by lacA and cysE. ;;
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                                                                                                                          plasmid
             homologous
                                                                                                                       of Rhizobium
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RL MOI. Microbiol. 3:1649-1651(1989).

CC 1- FUNCTION: ACETYLTRANSFERASE INFLICATED IN THE O-ACETYLATION OF CC NO PACTORS.

CC NO PACTORS.

CC NO PACTORS.

CC ACETYLTRANSFERASES TO THE CYSE/LACA/LPXA/NODL FAMILY OF CC This SWISS-PROT entry is copyright. It is produced through a collaboration oc between the Swiss Institute of Bioinformatics and the EMBL outstation cc the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial cc entitles requires a license agreement (See http://www.isb.sib.ch/announce/cc or send an email to licensee(sb-sib.ch).

CC EMBL; X17557; CAA35590.1; -.

CC EMBL; X17557; CAA35590.1; -.

CC REMBL; Y00548; CAA66625.1; -.

DR PIR; S01039; S01039.

DR PIR; S07000; S07000.

DR PIR; S07000; Lexapep; 2.

PFAN; PF001123; hexapep; 2.

DR PFAN; PF001123; hexapep; 2.

DR PFAN; PF001123; hexapep; 3.

PFAN; PF001123; hexapep; 2.

DR PROSITE; PS00101; HEXAPEP TRANSFERASES; 1. Length 190; Best Local Similarity 42.7%; Pred. No. 3.1e-06; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3; Mismatches 39; Indels 7; Gaps 3; Mismatches 44; Conservative 13; Mismatches 14; Mismatches 14; Mismatches 14; Mismatches 14; Mismatches 14; Mismatc
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